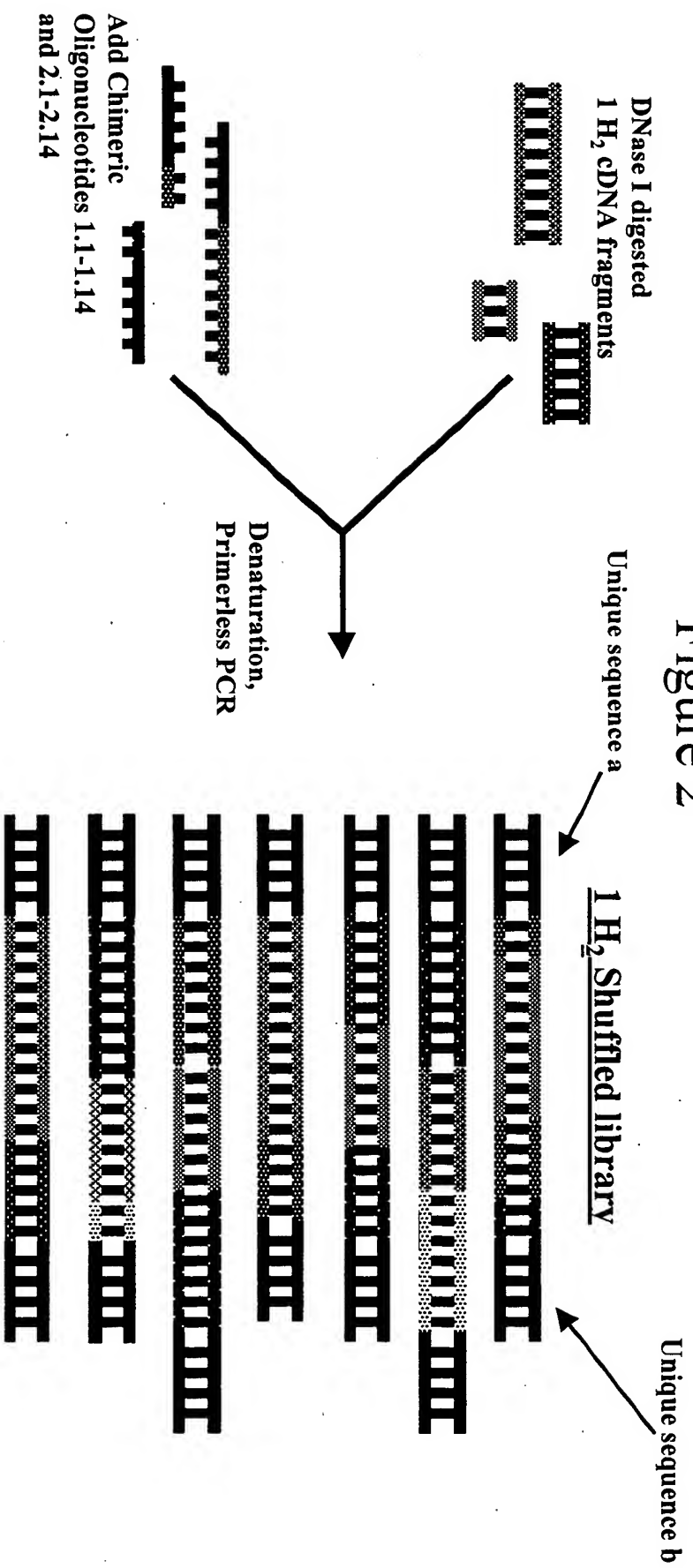


Figure 1

Figure 2



Shuffled 2H<sub>2</sub>, 3H<sub>2</sub>, 4H<sub>2</sub>, and 5H<sub>2</sub> libraries are created through the same method using chimeric oligonucleotides 3.1-3.14/4.1-4.14, 5.1-5.14/6.1-6.14, 7.1-7.14/8.1-8.14 and 9.1-9.14/10.1-10.14, respectively. Sequences 2 H<sub>2</sub>, 3 H<sub>2</sub>, 4 H<sub>2</sub>, and 5 H<sub>2</sub> are flanked by unique sequences c and d, e and f, g and h, and i and j, respectively.

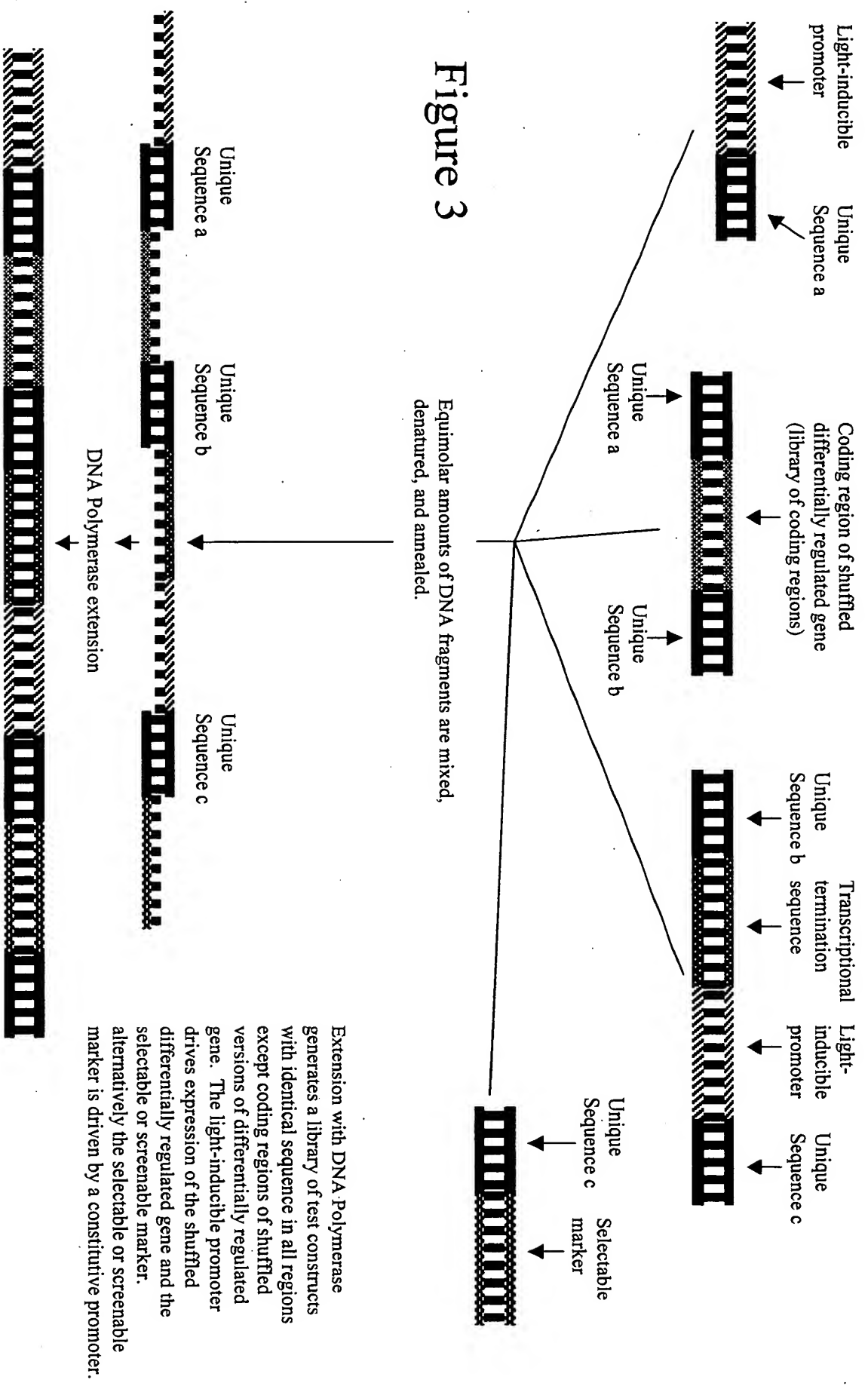
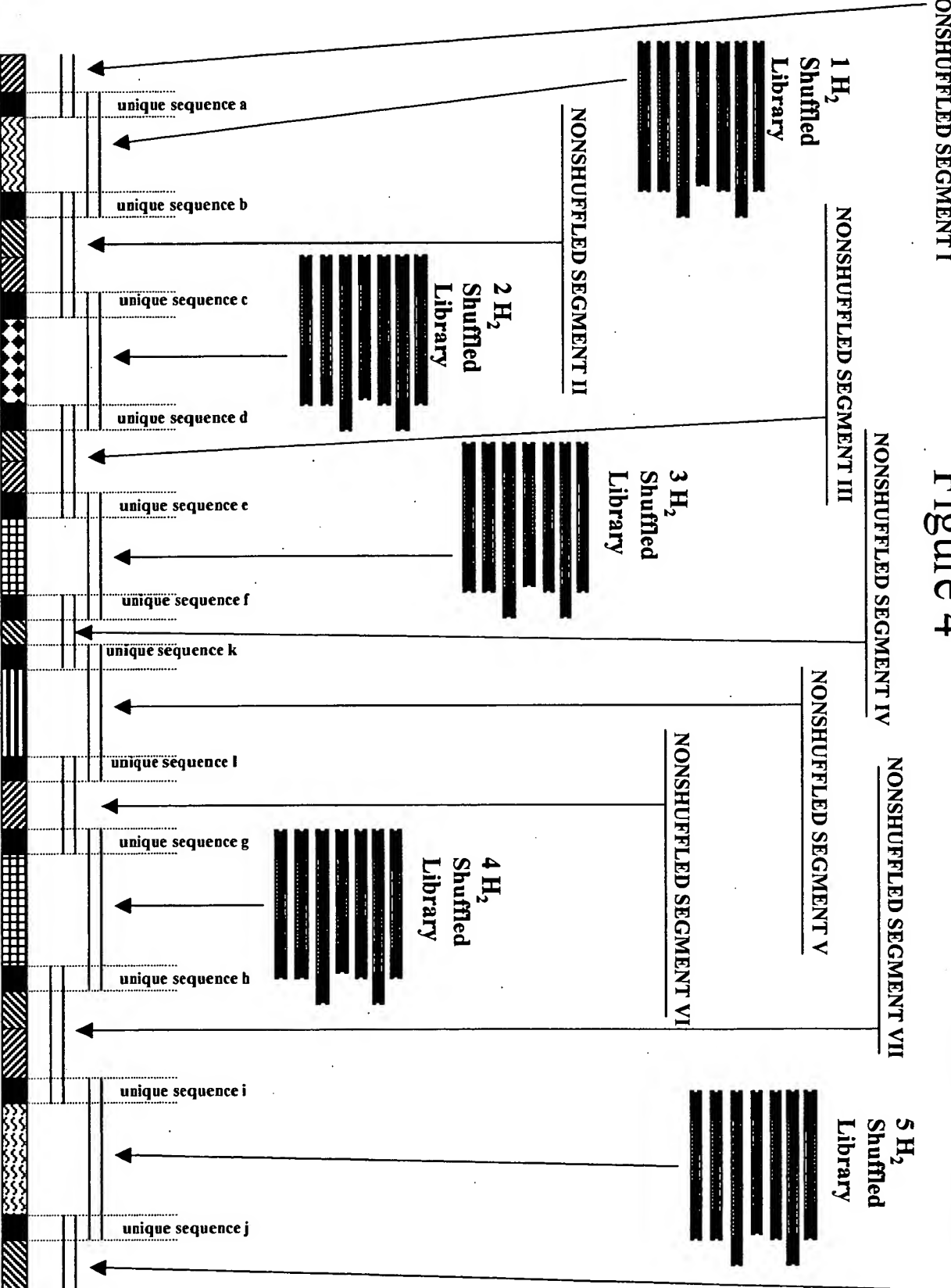


Figure 3

## NONSHUFFLED SEGMENT I

Figure 4

## NONSHUFFLED SEGMENT VIII

1-5 H<sub>2</sub> test construct map

# Figure 5

1-5 H<sub>2</sub> test constructs

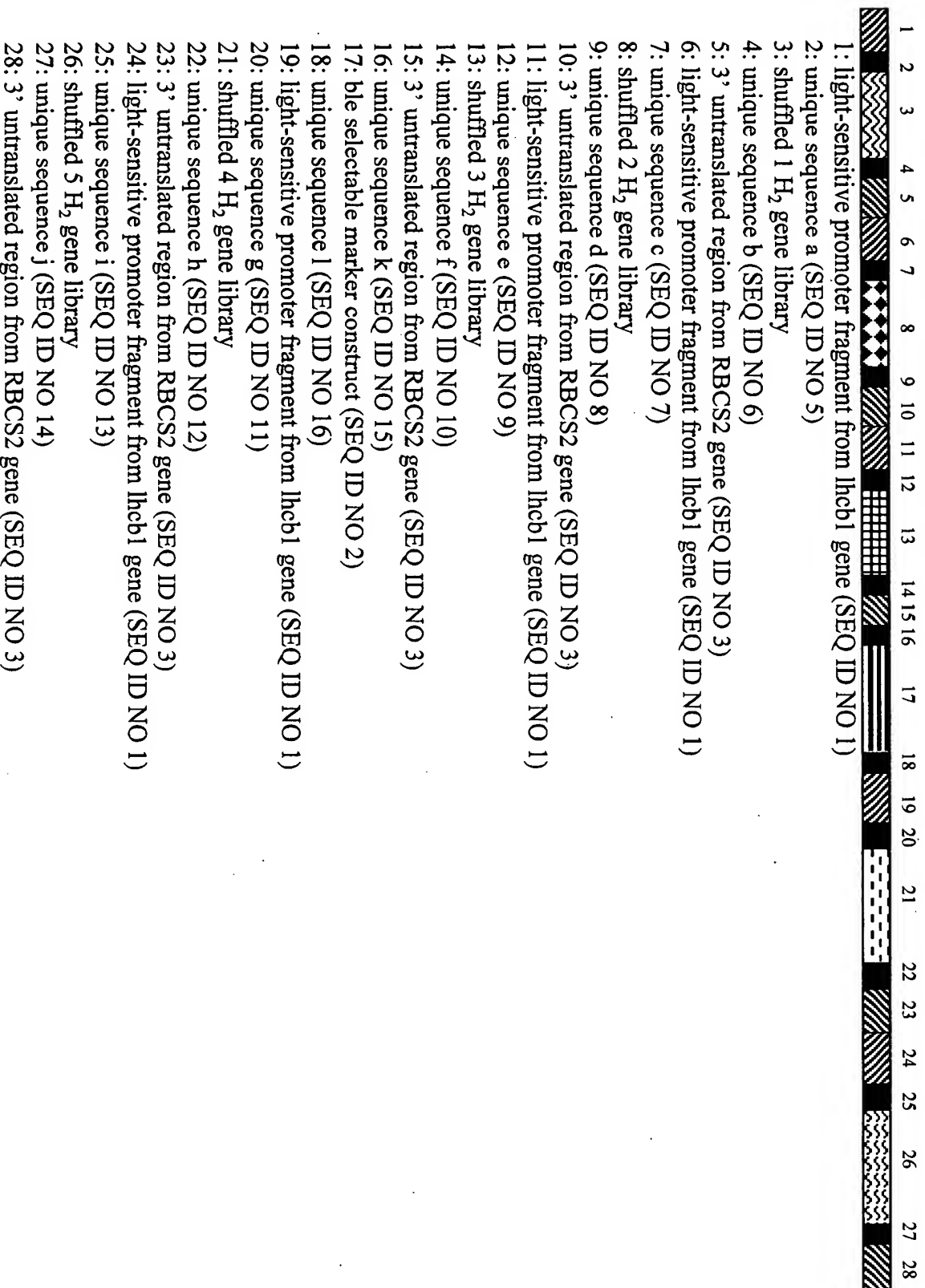
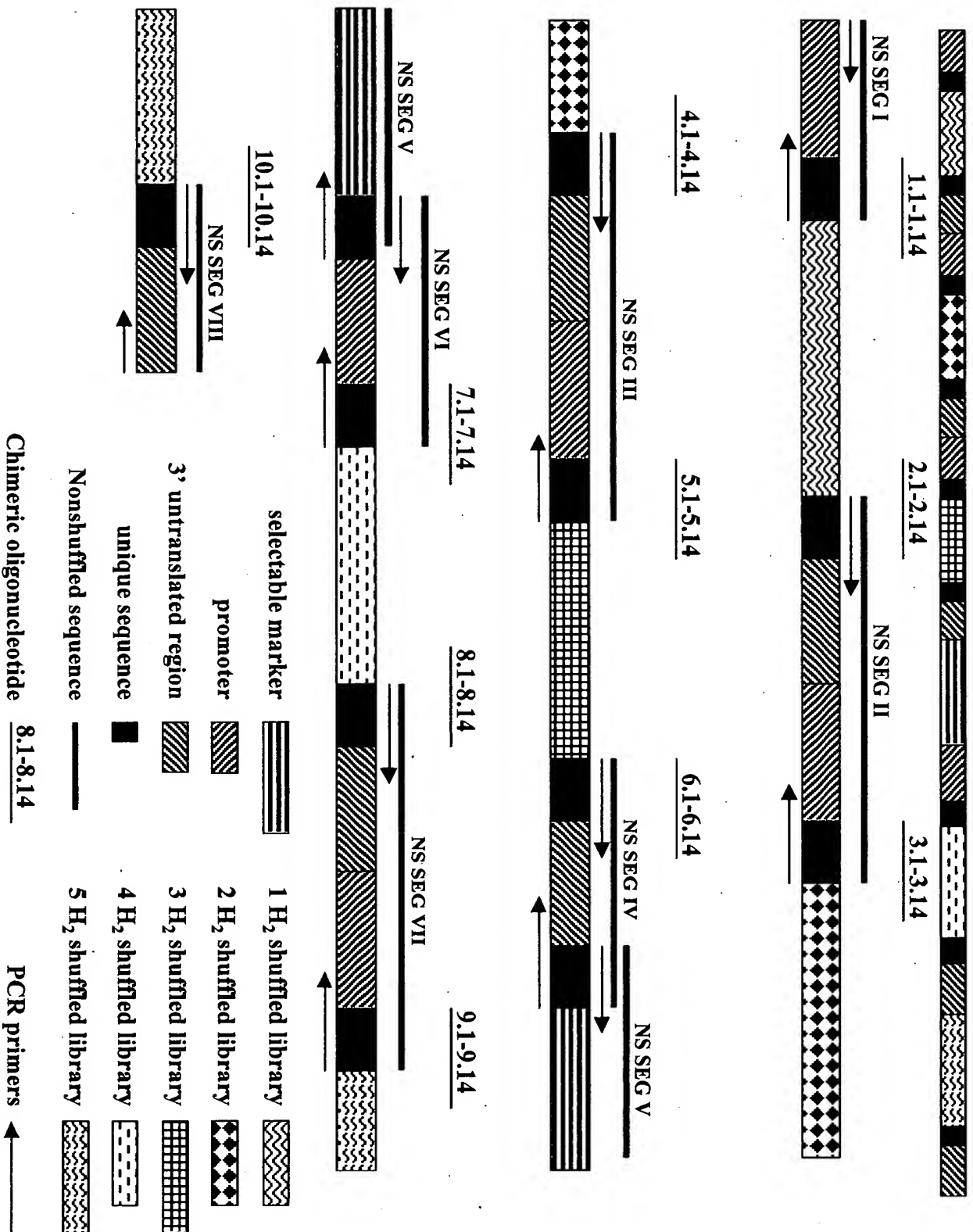
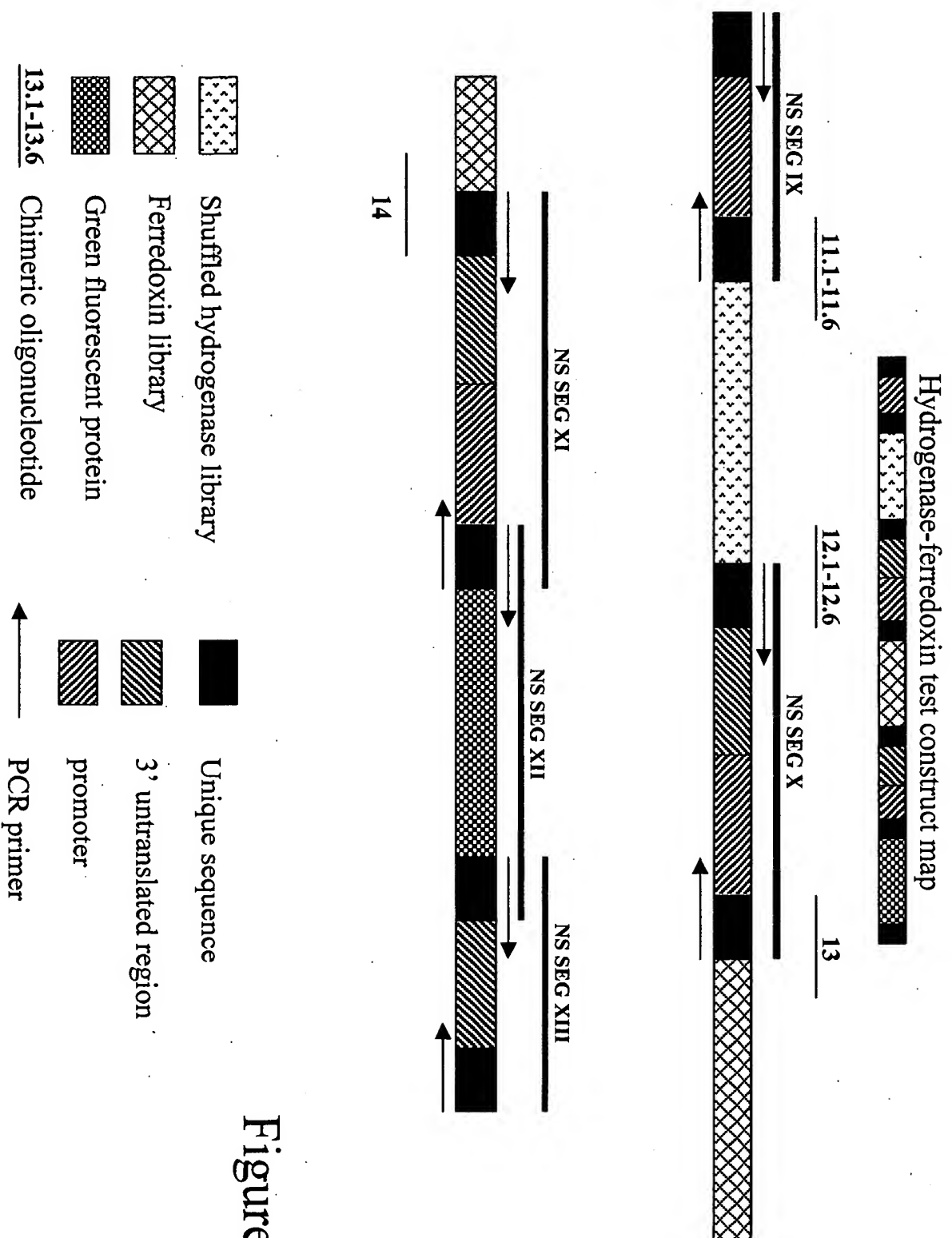


Figure 6





**Figure 8**

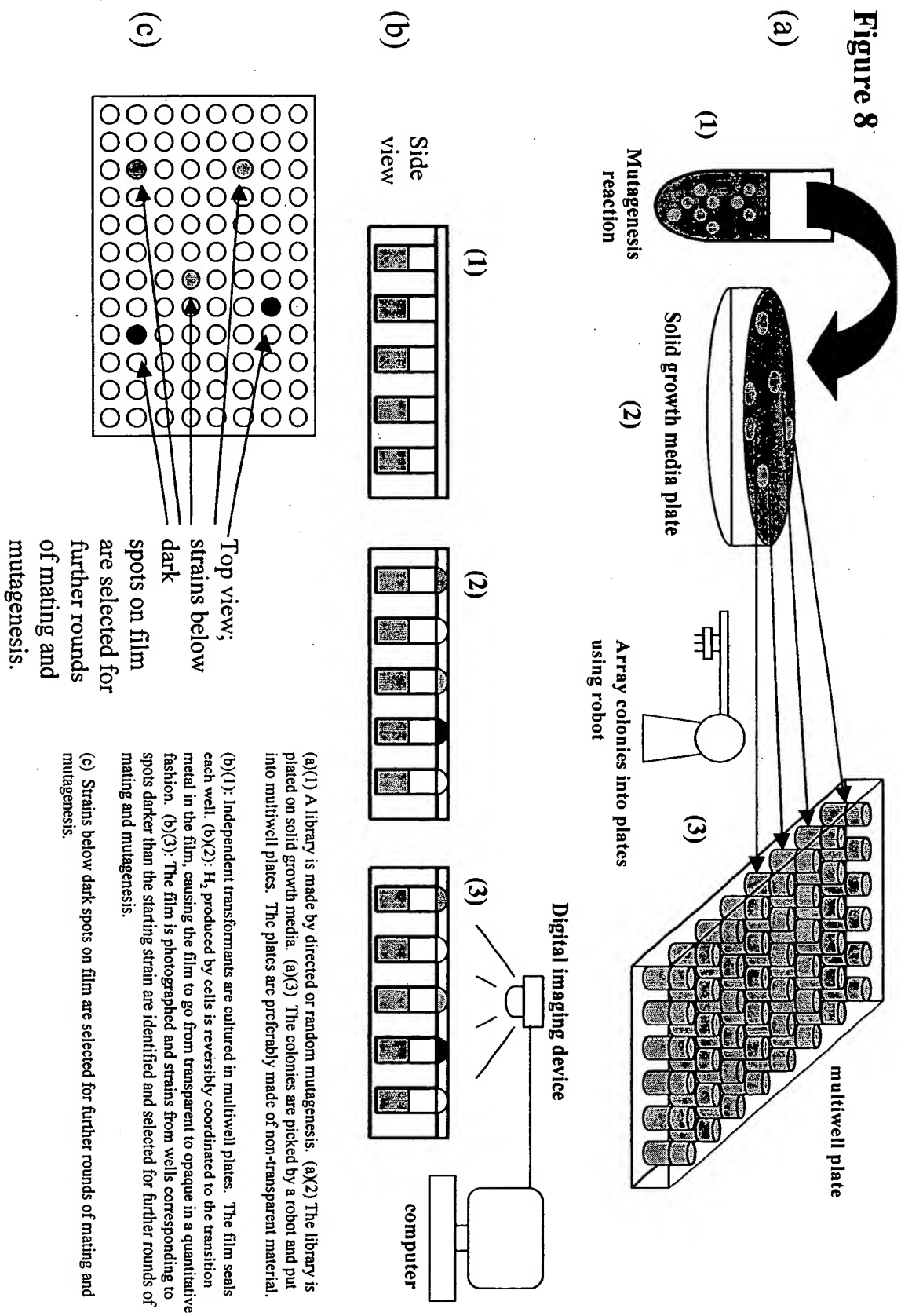
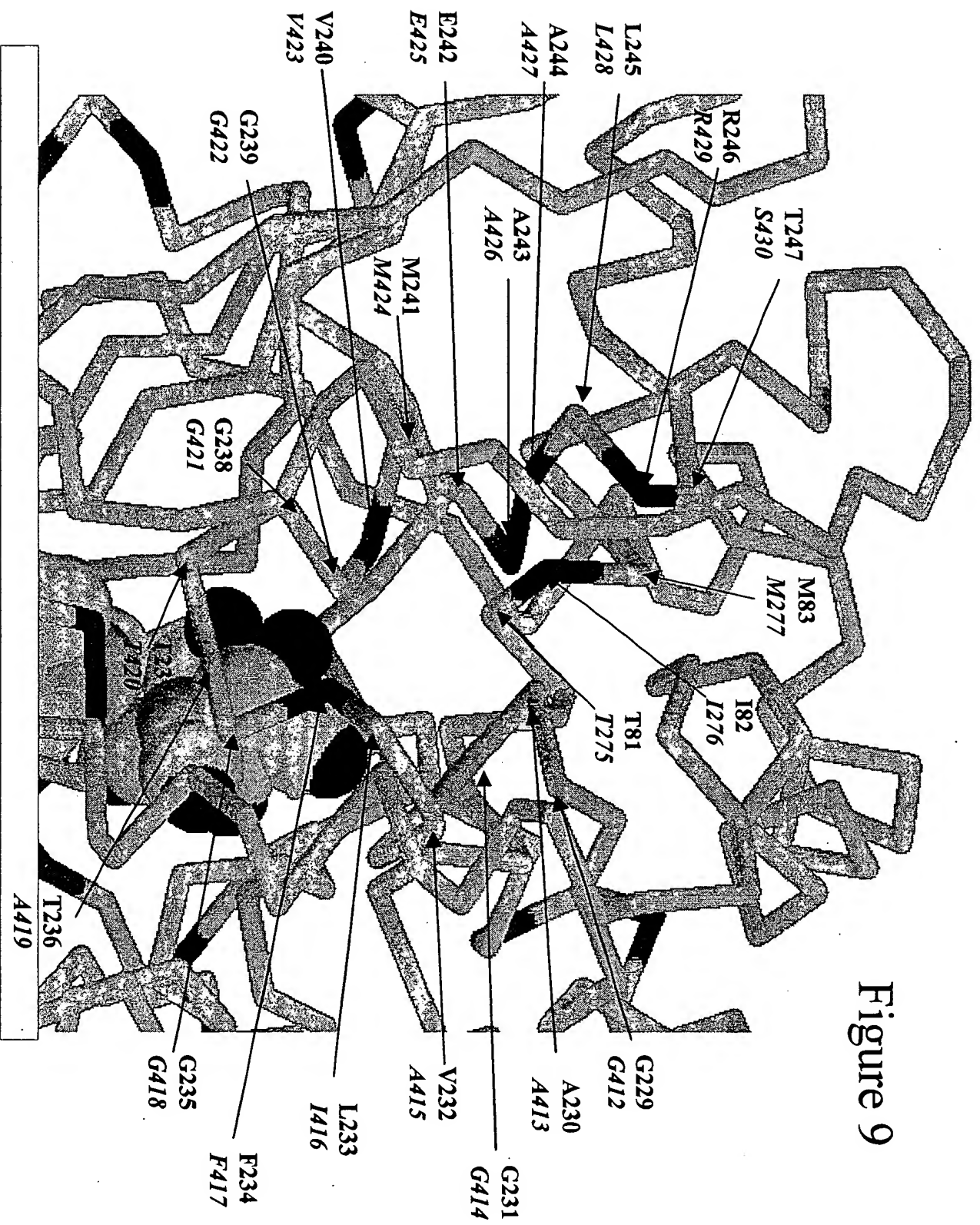




Figure 9

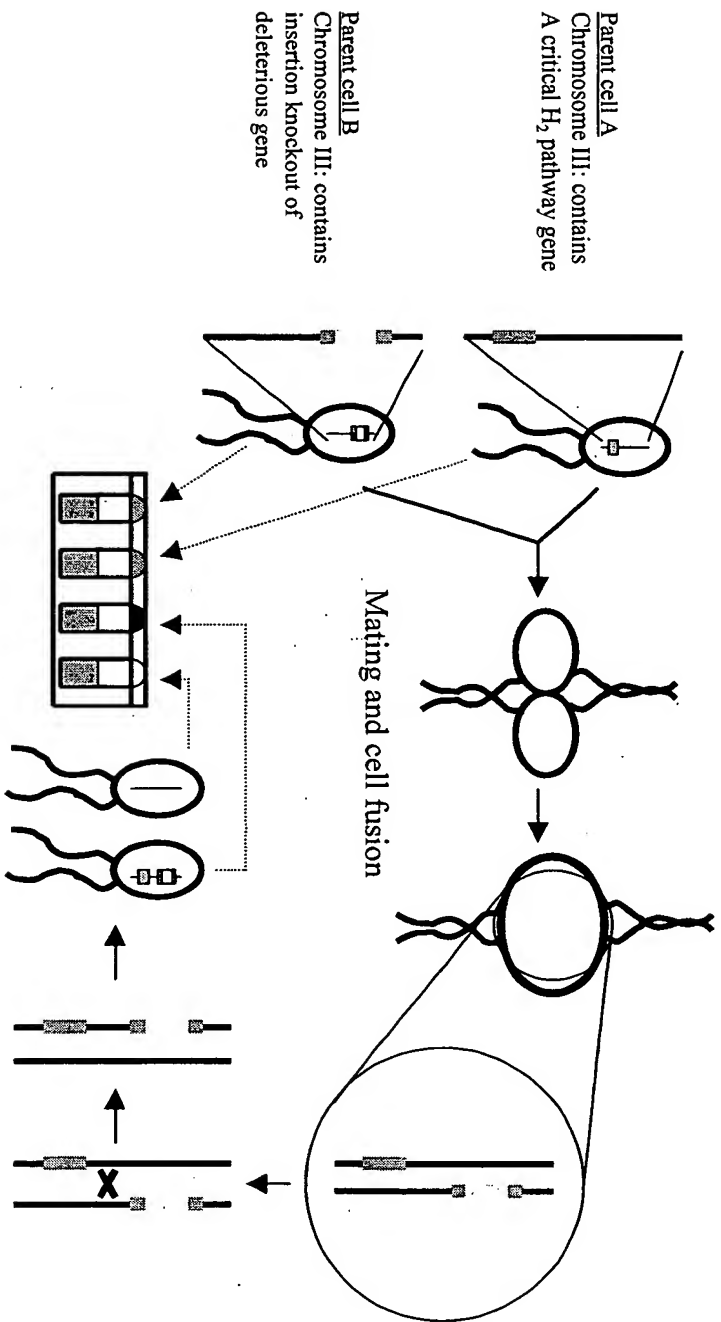


# Figure 10

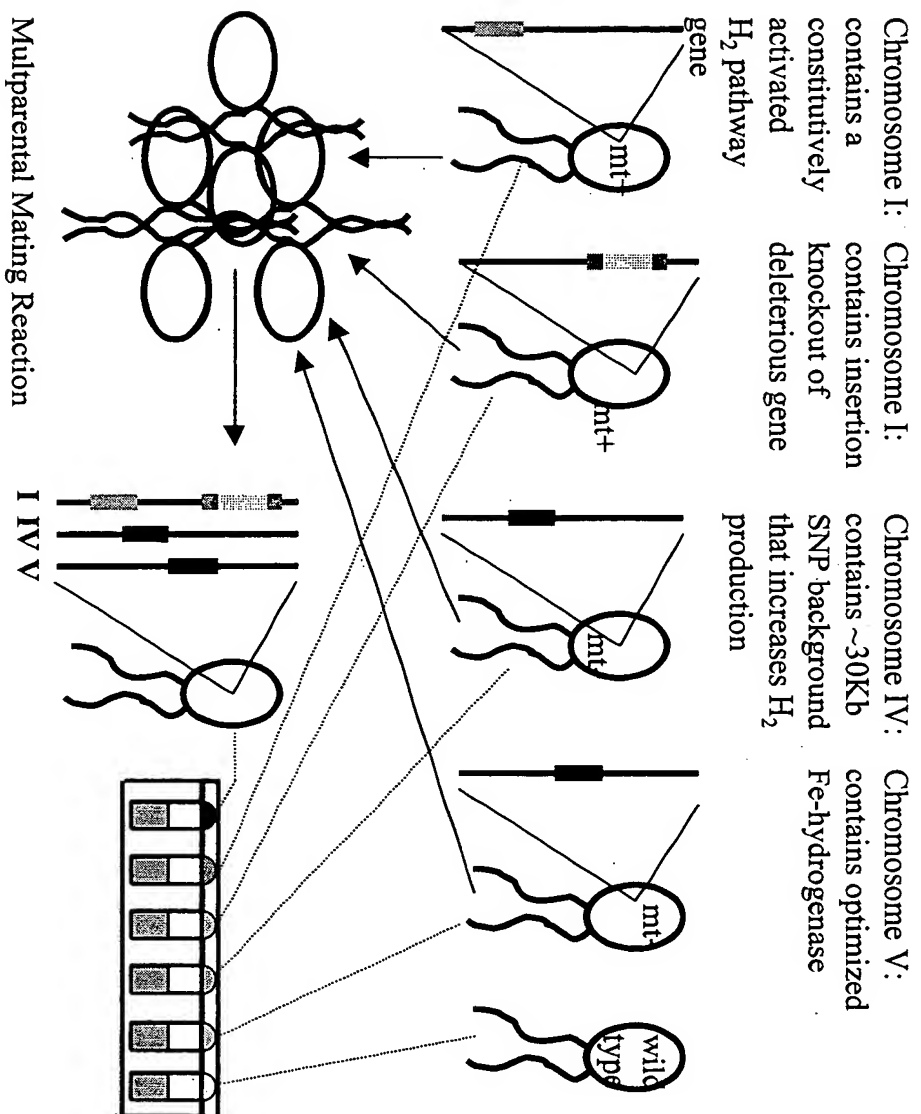
C. Reinhardtii Codon Usage Table: most preferred codons  
are shown underlined and in bold-face type

TTT 4.8 Phe	TCT 4.7 Ser	TAT 2.6 Tyr	TGT 1.4 Cys
<u>TTC 29.0 Phe</u>	TCC 16.8 Ser	<u>TAC 23.8 Tyr</u>	<u>TGC 12.8 Cys</u>
TTA 0.7 Leu	TCA 3.0 Ser	<u>TAA 1.2 STOP</u>	TGA 0.5 STOP
TTG 3.7 Leu	TCG 16.2 Ser	TAG 0.4 STOP	<u>TGG 13.5 Trp</u>
CTT 4.5 Leu	CCT 7.1 Pro	CAT 2.3 His	CGT 5.2 Arg
CTC 12.4 Leu	<u>CCC 29.9 Pro</u>	<u>CAC 17.5 His</u>	<u>CGC 35.3 Arg</u>
CTA 2.4 Leu	CCA 4.4 Pro	CAA 4.2 Gln	CGA 1.8 Arg
<u>CTG 65.4 Leu</u>	CCG 18.6 Pro	<u>CAG 36.2 Gln</u>	CGG 9.7 Arg
ATT 9.0 Ile	ACT 5.6 Thr	AAT 2.8 Asn	AGT 2.4 Ser
<u>ATC 28.0 Ile</u>	<u>ACC 29.9 Thr</u>	<u>AAC 29.9 Asn</u>	<u>AGC 20.8 Ser</u>
ATA 0.9 Ile	ACA 3.7 Thr	AAA 2.2 Lys	AGA 0.6 Arg
<u>ATG 26.8 Met</u>	ACG 14.7 Thr	<u>AAG 46.6 Lys</u>	AGG 2.5 Arg
GTT 5.3 Val	GCT 17.6 Ala	GAT 7.0 Asp	GGT 10.3 Gly
GTC 16.3 Val	<u>GCC 55.2 Ala</u>	<u>GAC 41.6 Asp</u>	<u>GGC 63.2 Gly</u>
GTA 2.0 Val	GCA 9.6 Ala	GAA 2.5 Gln	GGA 4.9 Gly
<u>GTG 45.6 Val</u>	GCG 38.6 Ala	<u>GAG 53.4 Gln</u>	GGG 8.3 Gly

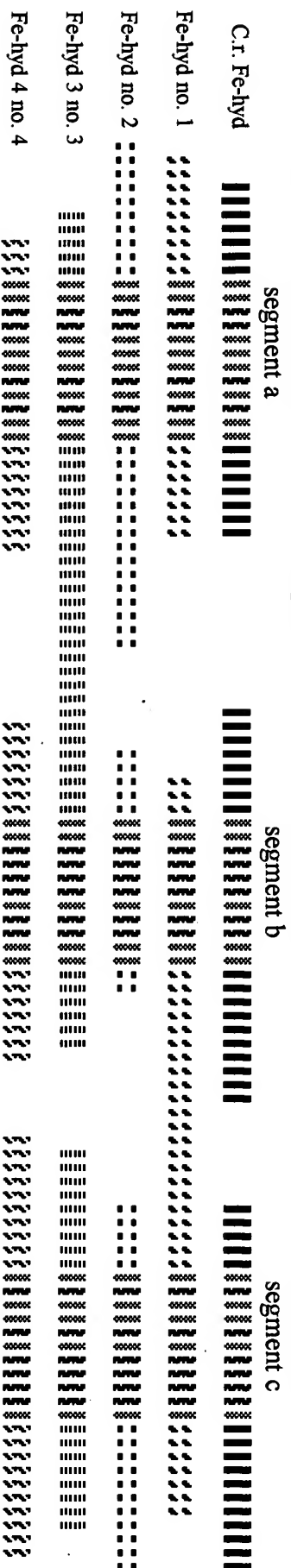
Figure 11



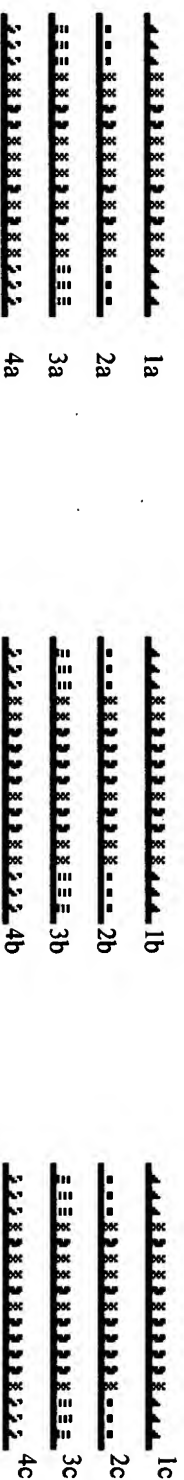
**Figure 12**



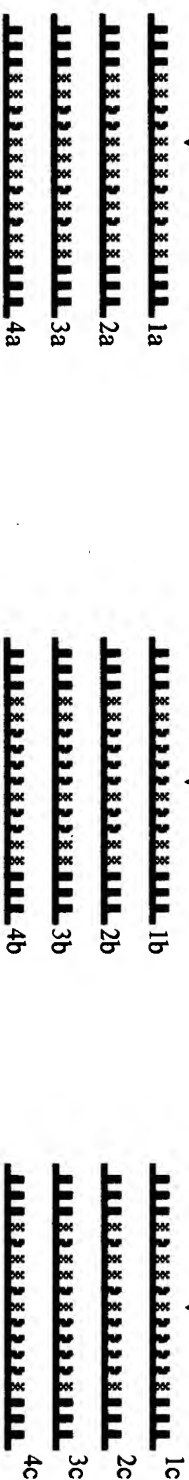
# Step 1 gas channel Figure 13



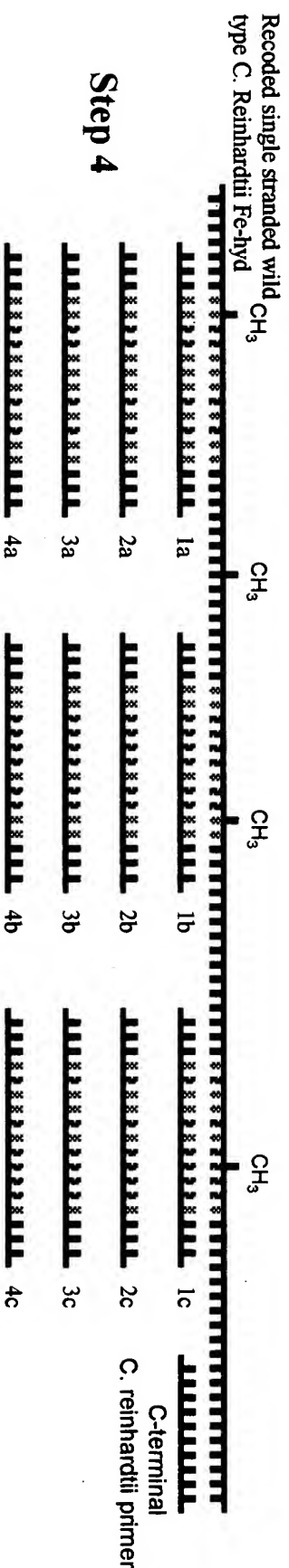
## Step 2



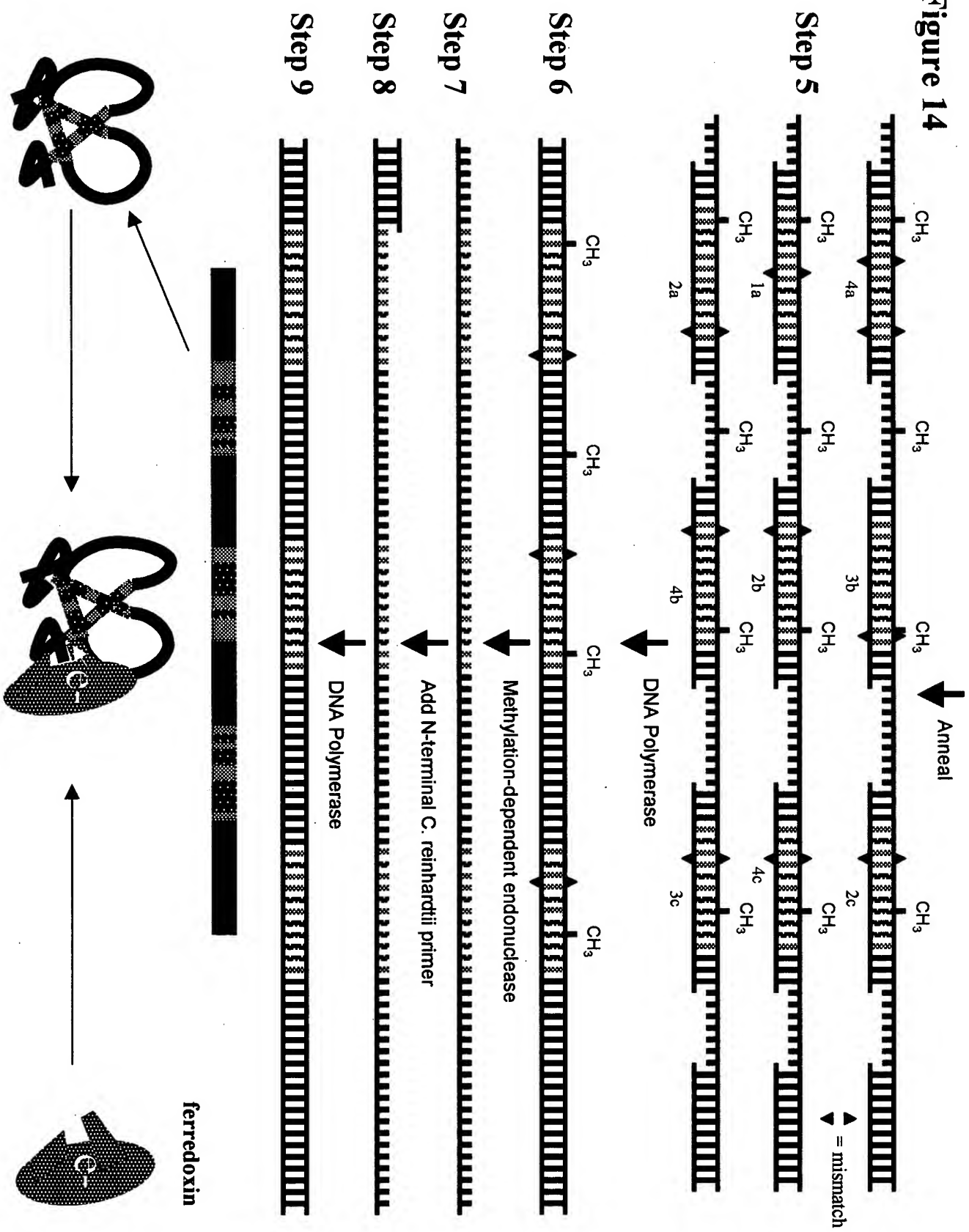
## Step 3



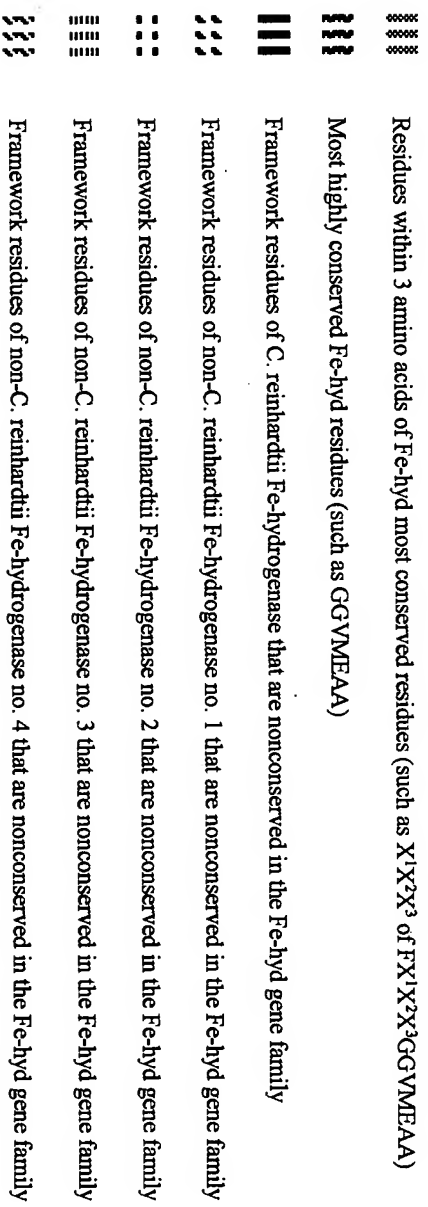
## Step 4



**Figure 14**



# Figure 15

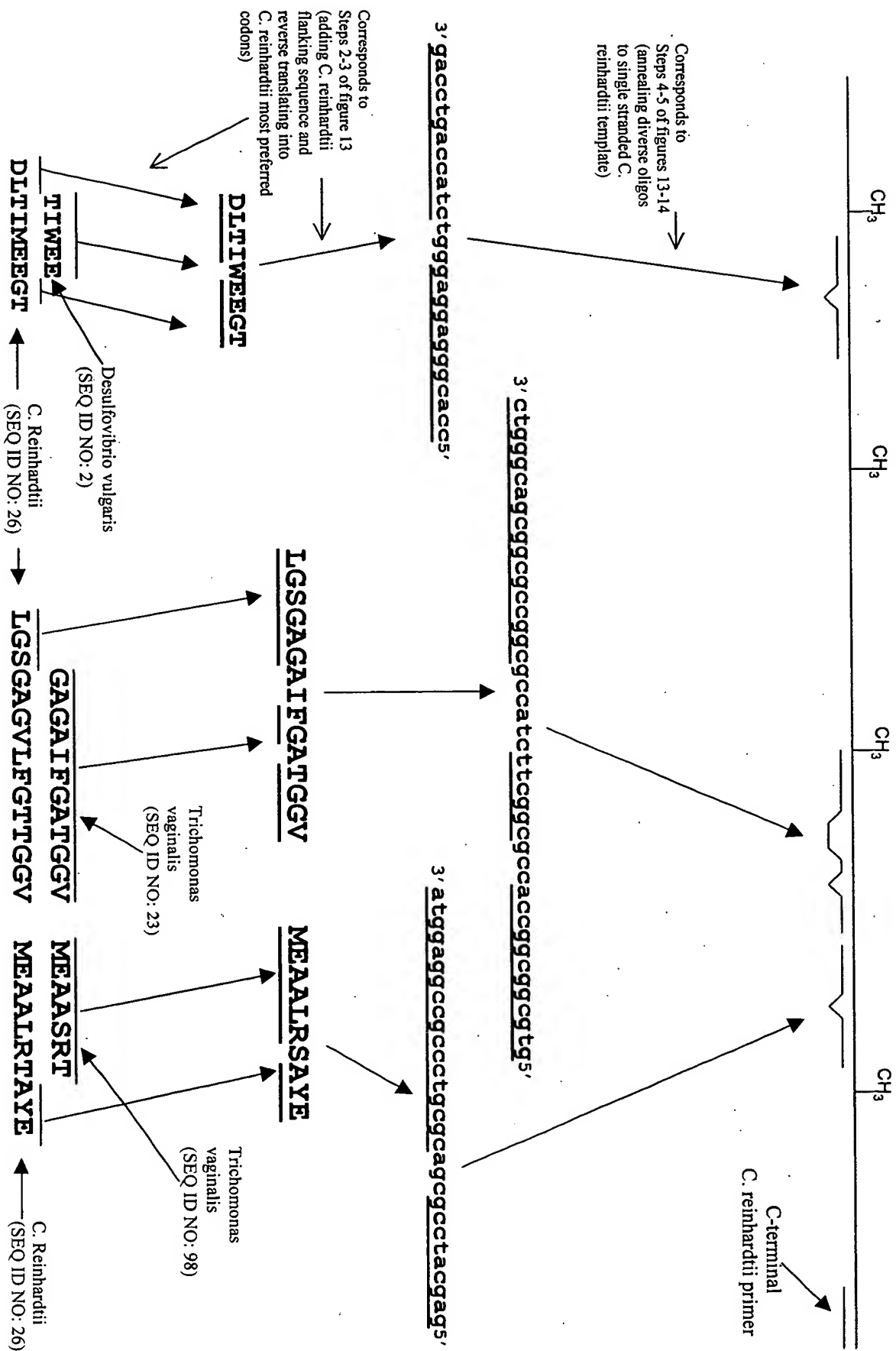


# Figure 16

<u>GCVMEAA Aligned Segments</u>		• <u>TIMEE Aligned Segments</u>	
<u>from SEQ ID NOs: 1-122:</u>		<u>from SEQ ID NOs: 1-122:</u>	
<u>(corresponding to SEQ ID Nos:</u>		<u>(corresponding to SEQ ID Nos:</u>	
<u>124-141)</u>		<u>142-147)</u>	
1.	GAGVIFGATGGVMEAAALRT	1.	TIMEE
2.	GGAIFCATGGVMEAAVRS	2.	TIVEE
3.	GGATIFGVTGGVMEAAALRF	3.	TIMEE
4.	GAGAIFGATGGVMEAAALRS	4.	TICEE
5.	GAGAIFGATGGVMEAAIRS	5.	VIMEE
6.	GAAVIFGVTGGVMEAAALRT	6.	TARLE
7.	GAGQIFAAATGGVMEAAASRT		
8.	GGVLEFGTTGGVMEAAALRT		
9.	GAAVIFGTTGGVMEAAALRT		
10.	GAAPIFGVTGGVIEAAALRT		
11.	GAGVIEGTTGGVMEAAALRS		
12.	GAGVIFGATGGVMEAAIIRT		
13.	SAGNLEFVTGGVMEAAIIRT		
14.	GAGAIFGATGGVMEAAALRT		
15.	GAGVLEFTTGGVMEAAALRT		
16.	GAAALEFVTGGVMEAAALRT		
17.	GAGVLEFTTGGVMEAAAVRT		
18.	GAGTIFGTTGGVMEAAALRT		



# Figure 17



Amplify promoters from genes  
in nuclear, chloroplast, and  
mitochondrial genomes

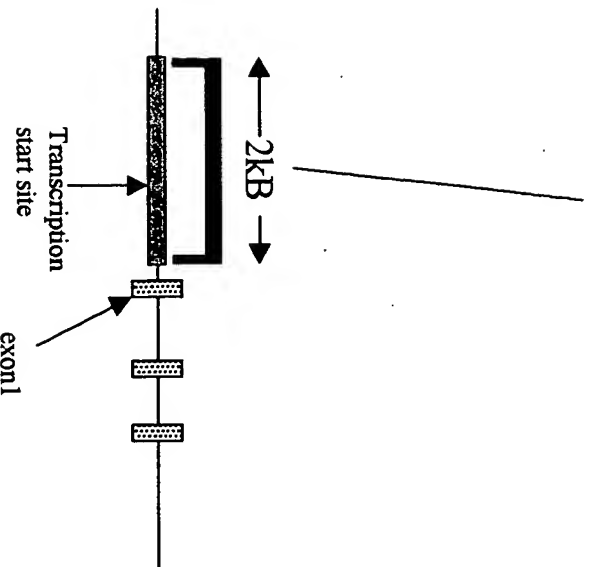
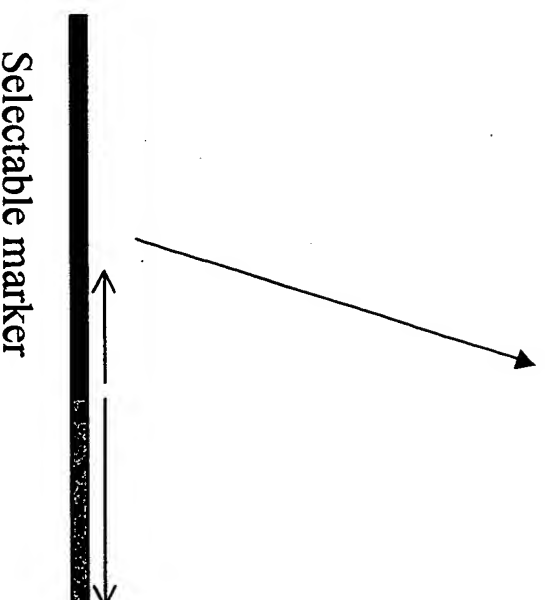


Figure 18

Make insertion library with diverse promoters and  
screen or select for desired phenotype that arises  
due to altered transcriptional regulation of  
metabolic pathway.



Selectable marker

Connect to selectable marker through  
chimeric oligonucleotides and  
DNA Polymerase extension (marker  
Gene is transcribed in opposite direction)